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TECH CENTER 1600/2900

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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/898,165B

DATE: 03/12/2003

TIME: 08:56:08

Input Set : A:\2d81552.txt

Output Set: N:\CRF4\03122003\I898165B.raw

P6

ENTERED

4 <110> APPLICANT: Daniel H. Cohn  
 5 Muhammad Faiyaz ul Haque  
 6 Lily M. King  
 7 Deborah Krakow  
 9 <120> TITLE OF INVENTION: 3-Phosphoadenosine-5-Phosphosulfate  
 10 (PAPS) Synthetase Proteins and Methods for Treating  
 11 Osteoarthritic Disorders  
 13 <130> FILE REFERENCE: 18810-81552  
 15 <140> CURRENT APPLICATION NUMBER: US 09/898,165B  
 16 <141> CURRENT FILING DATE: 2001-07-02  
 18 <150> PRIOR APPLICATION NUMBER: 09/399,212  
 19 <151> PRIOR FILING DATE: 1999-09-17  
 21 <160> NUMBER OF SEQ ID NOS: 33  
 23 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
 25 <210> SEQ ID NO: 1  
 26 <211> LENGTH: 2014  
 27 <212> TYPE: DNA  
 28 <213> ORGANISM: Homo sapiens  
 30 <400> SEQUENCE: 1  
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 32 ctccgcccga gccagccagc atgtcgggga tcaagaagca aaagacggag aaccacgaga 120  
 33 aatccaccaa tggtagtctat caggcccacc atgtgagcag gaataagaga gggcaagtgg 180  
 34 ttggaacaag gggtggttc cgaggatgtc cctgtggct aacaggcttc tctgtgtctg 240  
 35 gaaaaacaac gataagttt gccctggagg agtacattgt ctcccatgcc atcccttgtt 300  
 36 actcccttggaa tggggacaat gtccgtcatg gccttaacag aaatctcgaa ttctctcctg 360  
 37 gggacagaga gggaaatatac cgccggattt ctgaggtggc taagctgttt gctgatgtctg 420  
 38 gtcgtgtctg cattaccagg tttatattctc cattcgcaaa ggatcgtgag aatgcccga 480  
 39 aaatacatga atcagcaggg ctgccattct ttgaaatatt tggtagatgca cctctaaata 540  
 40 ttgtgaaag cagagacgtt aaaaaggcc cagagctggg gagattaaag 600  
 41 gatttacagg tattgattct gattatgaga aacctgaaaac tcctgagcgt gtgcattaaaa 660  
 42 ccaatttgcacatcacgtt gactgtgtcc accaggtgtt ggaacttctg caagagcaga 720  
 43 acattgttacc ctatactata atcaaagata tccacgaact ctttgtgccc gaaaacaaac 780  
 44 ttgaccacgtt ccgagctgag gctgaaactt tcccttcattt atcaattact aagctggatc 840  
 45 tccagtgggtt ccaggttttgc agcgaaggctt gggccactcc cctcaaaagggtt ttcattgcggg 900  
 46 agaaggagta ttacaggtt atgcactttt acaccctgtt agatgtatggc gtgatcaaca 960  
 47 tgacatccc cattgtactt cccgtctctg cagaggataa gacacggctg gaagggtgca 1020  
 48 gcaagttgtt cctggcacat ggtggacgga gggtagctat cttacgagac gctgaattct 1080  
 49 atgaacacag aaaagaggaa cgtgttccc gtgttgggg gacaacatgt acaaaacacc 1140  
 50 cccatatacaa aatggtgatg gaaagtgggg actggctgtt tggggagac cttcagggtgc 1200  
 51 tggagaaaat aagatgaaat gatgggctgg accaataccg tctgacacactt ctggagctca 1260  
 52 aacagaaaatg taaagaaaatg aatgctgtat cgggtttgc attccagtttgc cgaatcctg 1320  
 53 tccacaatgg ccatgccttgc ttgtatgcagg acacctgccg caggctccta gagagggct 1380  
 54 acaagcaccc ggtccttcta ctacaccctc tggggctg gaccaaggat gacgatgtgc 1440

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55 ctcttagactg gcggatgaag cagcacgcgg ctgtgctcg aagaagggtc ctggatccca 1500  
 56 agtcaaccat tggccatc ttccgtctc ccatgtata tgctggccccc acagagggtcc 1560  
 57 agtggcactg caggtcccg agtattgcgg gtgccaattt ctacattgtg gggagggacc 1620  
 58 ctgcaggaat gccccatcct gaaaccaaga aggatctgt a tgaacccact catggggca 1680  
 59 aggtcttgag catggccctt ggcctcacct ctgtgaaat cattccatc cgagtggctg 1740  
 60 cctacaacaa agccaaaaaa gccatggact tctatgatcc agcaaggcac aatagatgg 1800  
 61 acttcatctc aggaactcga atgaggaagc tcgccccggg aggagagaat ccccccagatg 1860  
 62 gcttcatggc ccccaaagca tgaagggtcc tgacagatta ttacagggtcc ctggagaaga 1920  
 63 actaaggcctt tgggtccaga gtttcttctt gaagtgcctt ttgattaccc tttcttatttt 1980  
 64 tatgattaga tgctttgtat taaattgctt ctca 2014  
 65 <210> SEQ ID NO: 2  
 66 <211> LENGTH: 2000  
 67 <212> TYPE: DNA  
 68 <213> ORGANISM: Mus musculus  
 69 <400> SEQUENCE: 2  
 70 gtattctcaa catcagatat catgtcttgg aggaagttac ctaaactctg aagaattatc 60  
 71 atgtctgcaa atttcaaaat gaaccataaa agagaccagc aaaaatccac caatgtggtc 120  
 72 taccaggccc atcatgtgag caaggaacaag agaggacaag tgggtggac cagggagga 180  
 73 ttccgaggat gtaccgtgt gctaacaggt ctctctggg ctggggaaaac aaccataagc 240  
 74 tttgctttgg aagagtaccc tttatctcac gccatccat gttactccct ggatggggac 300  
 75 aatgtccgtc atggccttaa taagaacctg ggattctctg ccggggaccg agaagagaat 360  
 76 atccgccccgga tcgccccggg ggccttgc tttgcgcacg ccggccttggg ttgcattcacc 420  
 77 agctttatct ctcctttgc aaaggatcg gagaatgcgg gaaaaatccca cgaatcagca 480  
 78 ggactcccggt tctttgagat cttttagat ggcctttaa atatctgtga aagccgagac 540  
 79 gtaaaaggac tctacaaacg agcccgagca ggagagatta aagggtttac aggcatcgat 600  
 80 tctgactatg agaaacctga aactcccgaaatgtgtctga agaccaactt gtctcagta 660  
 81 agcgactgtg tgcaacaggt ggtggactt ttgcaggacg agaacattgt accccacacc 720  
 82 accatcaaag gcatccacga actctttgtt ccagaaaaca aagtcgatca aatccgagct 780  
 83 gaggcagaga ctctccatc actaccaattt accaagctgg atctgcagtg ggtgcagatt 840  
 84 ctgagtgaag gctggccac tcccttcaaa ggctttatgc gggagaagga atacttgca 900  
 85 actctacact tcgacactct actggacatg ggagtcatca acatgagtat tcccttgc 960  
 86 ttggccgttt ctgcgtatga caaggcacgg ctcgaagggt gcagcaattt tgccttgc 1020  
 87 tacaaagggtc ggagggtcgc tctattacag gaccctgaat tctatgagca taggaaagag 1080  
 88 gacgtttgtt ctcgtgtgt gggacacagcc actgcaaagc acccccatat caaaatggtg 1140  
 89 atggaaagtg gggactggct tttgggtgg gacctacagg tgcttagagag aataagggtgg 1200  
 90 gacgtgggc tggaccaata ccgccttacg cctctggac tcaaacagaaa gtgtaaagac 1260  
 91 atgaatgctg atgcgtgtt tgcattccag ttgcgcatac ctgtccacaa tggcatgccc 1320  
 92 ctccgtatgc aggacaccccg ccgcaggctc ctggagaggg gttacaagca cccagtcctc 1380  
 93 ctgtccacc ctcttgggg ctggaccaag gacgtgacg tacctctggat atggaggatg 1440  
 94 aaacagcatg cagctgtact ggaggaaagg gtcctggatc ccaagtcaac tattttggcc 1500  
 95 atctttccat ctccatgtt atacgctgtt cccacagagg tccagtgcc ttgcagatgc 1560  
 96 cggatgattg caggagccaa ttctacattt gtgggttaggg atcccgccagg aatccccat 1620  
 97 cctgagacaa agaaagaccc atatgaaccc acccacgggg gcaagggtctt ggtatggcc 1680  
 98 cctggccctta cctctgtgg aataattccg ttccgagtggtt ctgcctacaa taaaattaaa 1740  
 99 aaggccatgg acttttatga tccagcaagg cacgaggagt ttgacttcat ctcaaggact 1800  
 100 cgcgtggatgg agctcgcccg ggaaggagaa gatccccat atggcttcat ggccccgaaa 1860  
 101 gctctggctt ctccatcaag tgctctctgtt cgtttttttt tttcttatttt tttttttttt 1920  
 102 ctgctctgtatcaag tccatcaag tccatcaag tccatcaag tccatcaag tccatcaag 1980  
 103 ctgctctgtatcaag tccatcaag tccatcaag tccatcaag tccatcaag tccatcaag 2000

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107 <210> SEQ ID NO: 3  
108 <211> LENGTH: 20  
109 <212> TYPE: DNA  
110 <213> ORGANISM: Homo sapiens  
112 <400> SEQUENCE: 3  
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115 <210> SEQ ID NO: 4  
116 <211> LENGTH: 20  
117 <212> TYPE: DNA  
118 <213> ORGANISM: Homo sapiens  
120 <400> SEQUENCE: 4  
121 cggaaagatg gcaacaatgg 20  
123 <210> SEQ ID NO: 5  
124 <211> LENGTH: 20  
125 <212> TYPE: DNA  
126 <213> ORGANISM: Homo sapiens  
128 <400> SEQUENCE: 5  
129 ctggtgctgg aaaaacaacg 20  
131 <210> SEQ ID NO: 6  
132 <211> LENGTH: 22  
133 <212> TYPE: DNA  
134 <213> ORGANISM: Homo sapiens  
136 <400> SEQUENCE: 6  
137 tgcgaatgga gaaataaagc tg 22  
139 <210> SEQ ID NO: 7  
140 <211> LENGTH: 615  
141 <212> TYPE: PRT  
142 <213> ORGANISM: Homo sapiens  
144 <400> SEQUENCE: 7  
145 Met Ser Gly Ile Lys Lys Gln Lys Thr Glu Asn Gln Gln Lys Ser Thr  
146 1 5 10 15  
147 Asn Val Val Tyr Gln Ala His His Val Ser Arg Asn Lys Arg Gly Gln  
148 20 25 30  
149 Val Val Gly Thr Arg Gly Gly Phe Arg Gly Cys Thr Val Trp Leu Thr  
150 35 40 45  
151 Gly Leu Ser Gly Ala Gly Lys Thr Thr Ile Ser Phe Ala Leu Glu Glu  
152 50 55 60  
153 Tyr Leu Val Ser His Ala Ile Pro Cys Tyr Ser Leu Asp Gly Asp Asn  
154 65 70 75 80  
155 Val Arg His Gly Leu Asn Arg Asn Leu Gly Phe Ser Pro Gly Asp Arg  
156 85 90 95  
157 Glu Glu Asn Ile Arg Arg Ile Ala Glu Val Ala Lys Leu Phe Ala Asp  
158 100 105 110  
159 Ala Gly Leu Val Cys Ile Thr Ser Phe Ile Ser Pro Phe Ala Lys Asp  
160 115 120 125  
161 Arg Glu Asn Ala Arg Lys Ile His Glu Ser Ala Gly Leu Pro Phe Phe  
162 130 135 140  
163 Glu Ile Phe Val Asp Ala Pro Leu Asn Ile Cys Glu Ser Arg Asp Val  
164 145 150 155 160

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165 Lys Gly Leu Tyr Lys Arg Ala Arg Ala Gly Glu Ile Lys Gly Phe Thr  
 166 165 170 175  
 167 Gly Ile Asp Ser Asp Tyr Glu Lys Pro Glu Thr Pro Glu Arg Val Leu  
 168 180 185 190  
 169 Lys Thr Asn Leu Ser Thr Val Ser Asp Cys Val His Gln Val Val Glu  
 170 195 200 205  
 171 Leu Leu Gln Glu Gln Asn Ile Val Pro Tyr Thr Ile Ile Lys Asp Ile  
 172 210 215 220  
 173 His Glu Leu Phe Val Pro Glu Asn Lys Leu Asp His Val Arg Ala Glu  
 174 225 230 235 240  
 175 Ala Glu Thr Leu Pro Ser Leu Ser Ile Thr Lys Leu Asp Leu Gln Trp  
 176 245 250 255  
 177 Val Gln Val Leu Ser Glu Gly Trp Ala Thr Pro Leu Lys Gly Phe Met  
 178 260 265 270  
 179 Arg Glu Lys Glu Tyr Leu Gln Val Met His Phe Asp Thr Leu Leu Asp  
 180 275 280 285  
 181 Asp Gly Val Ile Asn Met Ser Ile Pro Ile Val Leu Pro Val Ser Ala  
 182 290 295 300  
 183 Glu Asp Lys Thr Arg Leu Glu Gly Cys Ser Lys Phe Val Leu Ala His  
 184 305 310 315 320  
 185 Gly Gly Arg Arg Val Ala Ile Leu Arg Asp Ala Glu Phe Tyr Glu His  
 186 325 330 335  
 187 Arg Lys Glu Glu Arg Cys Ser Arg Val Trp Gly Thr Thr Cys Thr Lys  
 188 340 345 350  
 189 His Pro His Ile Lys Met Val Met Glu Ser Gly Asp Trp Leu Val Gly  
 190 355 360 365  
 191 Gly Asp Leu Gln Val Leu Glu Lys Ile Arg Trp Asn Asp Gly Leu Asp  
 192 370 375 380  
 193 Gln Tyr Arg Leu Thr Pro Leu Glu Leu Lys Gln Lys Cys Lys Glu Met  
 194 385 390 395 400  
 195 Asn Ala Asp Ala Val Phe Ala Phe Gln Leu Arg Asn Pro Val His Asn  
 196 405 410 415  
 197 Gly His Ala Leu Leu Met Gln Asp Thr Cys Arg Arg Leu Leu Glu Arg  
 198 420 425 430  
 199 Gly Tyr Lys His Pro Val Leu Leu His Pro Leu Gly Gly Trp Thr  
 200 435 440 445  
 201 Lys Asp Asp Asp Val Pro Leu Asp Trp Arg Met Lys Gln His Ala Ala  
 202 450 455 460  
 203 Val Leu Glu Glu Gly Val Leu Asp Pro Lys Ser Thr Ile Val Ala Ile  
 204 465 470 475 480  
 205 Phe Pro Ser Pro Met Leu Tyr Ala Gly Pro Thr Glu Val Gln Trp His  
 206 485 490 495  
 207 Cys Arg Ser Arg Met Ile Ala Gly Ala Asn Phe Tyr Ile Val Gly Arg  
 208 500 505 510  
 209 Asp Pro Ala Gly Met Pro His Pro Glu Thr Lys Lys Asp Leu Tyr Glu  
 210 515 520 525  
 211 Pro Thr His Gly Gly Lys Val Leu Ser Met Ala Pro Gly Leu Thr Ser  
 212 530 535 540  
 213 Val Glu Ile Ile Pro Phe Arg Val Ala Ala Tyr Asn Lys Ala Lys Lys

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560  
555 550  
575 565 570  
590 585 580  
605 600 595  
615 610  
8 617  
PRT  
Mus musculus  
SEQUENCE: 8  
15  
10 5  
30 25 35  
45 40 35  
60 55 50  
80 75 70  
95 90 85  
110 105 100  
125 120 115  
140 135 130  
160 155 150  
175 170 165  
190 185 180  
205 200 195  
220 215 210  
240 235 230  
255 250 245  
255 250 245  
270 265 260  
264 Met Arg Glu Lys Glu Tyr Leu Gln Thr Leu His Phe Asp Thr Leu Leu  
265

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**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:29; N Pos. 23,305